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Practitioner's Docket No. MPI00-535OMNICN1M

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Fraser, Christopher C., et al.		
Application No.:	10/741,790	Group No.:	1646
Filed:	December 19, 2003	Examiner:	Jiang, Dong
For:	NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES		

**Mail Stop Amendment**

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

**RESPONSE TO RESTRICTION REQUIREMENT**

Dear Sir:

Responsive to the Restriction Requirement dated November 1, 2006, the claims of Group I (claims 86-92 and 95-101), drawn to "an antibody specific to said polypeptides, and a method of making thereof", are elected for prosecution with traverse. The Examiner further requested that Applicants elect one specific polypeptide from the following: SEQ ID NO:417 and 419. In order to be fully responsive, Applicants elect SEQ ID NO:419 with traverse. Finally, the Examiner has requested that Applicants elect a species of detectable labels. Applicants elect the

**CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10\***

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species “radioactive material”. Claims readable on the elected species are claims 91, 92, 100 and 101.

Applicants hereby reserve the right to traverse the above restriction with respect to non-elected Groups II-IV in this or subsequent applications.

#### GROUND FOR TRAVERSAL

The Examiner states that the application contains multiple independent and patentably distinct inventions within Group A (i.e., the Examiner has required Applicants to elect either SEQ ID NO:417 or SEQ ID NO:419) and has required restriction under 35 U.S.C. § 121.

The Examiner has required election of a single sequence on the basis that “Each of SEQ ID NOs represents a unique and separately patentable sequence, requiring a unique search of the prior art. Searching all of the sequences in a single patent application would constitute an undue search burden on the examiner and the USPTO’s resources because of the non-coextensive nature of these searches.” Applicants note, however, that SEQ ID NO:417 corresponds to the full length form of TANGO294, which is 423 amino acids in length, whereas SEQ ID NO:419 corresponds to the mature form of TANGO294, which is 390 amino acids in length. The only difference between the sequence of SEQ ID NO:417 and that of SEQ ID NO:419 is that a 33 amino acid signal peptide is missing from the sequence depicted in SEQ ID NO:419. Therefore, applicants respectfully request that both SEQ ID NO:417 and SEQ ID NO:419 be searched in this application since a search of SEQ ID NO:419 necessarily encompasses a search of SEQ ID NO:417. Applicants submit that a search of both sequences would not place an undue search burden on the Examiner.

Furthermore, the proposed regrouping comports with the United States Patent Office Procedure as stated in the Manual of Patent Examination Procedure:

If the search and examination of an entire application can be made without serious burden, the Examiner must examine it on the merits, even though it includes claims to independent or distinct inventions (M.P.E.P § 803 at 800-3 (8<sup>th</sup> ed., Aug 2001)).